

GenCore version 5.1.6  
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OM protein - protein search, using swi model

Run on: June 25, 2003, 14:38:41 ; Search time 27.1047 Seconds  
(without alignments)  
843.812 Million cell updates/sec

Title: US-09-622-613B-17  
Perfect score: 605  
Sequence: 1 MQNMAFFQOKHINTPICN.....ICVNCENQYVHFAGIGRCP 111

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

```
Database :
SPREMBL_21.*
1: sp.archae.*
2: sp.bacteria.*
3: sp.fungi.*
4: sp.human.*
5: sp.invertebrate.*
6: sp.mammal.*
7: sp.jmhc.*
8: sp.organelle.*
9: sp.phage.*
10: sp.plant.*
11: sp.podent.*
12: sp.virus.*
13: sp.yeast.*
14: sp.unclassified.*
15: sp.virus.*
16: sp.bacteriap.*
17: sp.archaeap.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	585.5	36.6	133	13	09PMW7	09PMW7 rana catesi
2	554.5	31.5	133	13	09SMW0	09SMW0 rana catesi
3	481.5	79.5	132	13	09BSM2	09BSM2 rana catesi
4	472.5	78.0	133	13	09BSL9	09BSL9 rana catesi
5	465.5	76.8	133	13	09BSL8	09BSL8 rana catesi
6	442.5	73.1	132	13	09BSM1	09BSM1 rana catesi
7	370	51.1	132	13	09DF78	09df78 rana catesi
8	271.5	45.5	127	13	0918V8	0918V8 rana pipie
9	271.5	44.8	127	13	08UVX5	08UVX5 rana pipie
10	240	39.6	129	13	09DFV6	09dfv6 rana catesi
11	223.5	36.9	128	13	09DFV8	09dfv8 rana catesi
12	230.5	36.4	128	13	09DFV7	09dfv7 rana catesi
13	211.5	34.9	128	13	09DFV5	09dfv5 rana catesi
14	157	25.9	169	13	09W738	09w738 xenopus laevis
15	125	20.6	170	6	Q9BEC1	Q9BEC1 triturus cristatus
16	120	19.8	150	11	Q8VD94	Q8VD94 berlymus bo

## ALIGNMENTS

17	119.5	19.7	163	6	09BDC2	09bdc2 antilocapra
18	118.5	19.6	163	6	09TVC0	09tvc0 ratius scrofa
19	118	19.5	150	11	08VD88	08vd88 ratius norv
20	116.5	19.2	144	6	09BH14	09bh14 antilocapra
21	114	18.8	150	11	08VD92	08vd92 ratius exul
22	110.5	18.2	152	11	08VD89	08vd89 ratius norv
23	109.5	18.1	119	6	09TV33	09tv33 bos taurus
24	108.5	17.9	124	6	095NE6	095ne6 bubalus bub
25	106.5	17.6	149	11	08VD95	08vd95 beylains bo
26	106	17.5	134	6	09BD93	09bd93 tragulus ja
27	105.5	17.4	152	11	08VD84	08vd84 ratius cliom
28	105.5	17.4	156	6	08SQ05	08sq05 jagochxiom
29	104.5	17.2	119	6	09TVC0	09tvc0 saguinus oe
30	104.5	17.2	119	6	09TV38	09tv38 eulmair ful
31	104.5	17.2	124	6	09T5T2	09t5t2 bos taurus
32	103.5	17.1	142	6	09BEC3	09bec3 tragulus ja
33	103.5	17.1	156	6	08SQ06	08sq06 ateles geof
34	103	17.0	124	6	09BEC2	09bec2 tragulus ja
35	102.5	16.9	124	6	08SQ08	08sq08 saimir sci
36	102.5	16.9	156	6	08SQ07	08sq07 saguinus oe
37	101.5	16.7	152	11	08VD90	08vd90 ratius fusc
38	100.5	16.6	116	6	097933	097933 piocenoide
39	100.5	16.6	149	11	08VD93	08vd93 ratius exul
40	99.5	16.4	116	6	097934	097934 pseudorca c
41	99.5	16.4	119	6	09TS06	09ts6 ceropithec
42	98.5	16.3	119	6	09TV32	09tv32 gorilla gor
43	98.5	16.3	124	6	09XS40	09xs40 camelus bac
44	98	16.2	158	6	08SP12	08sp12 callithrix
45	97.5	16.1	158	6	08SP13	08sp13 saguinus la

## RESULT 1

ID	09PMW7	PRELIMINARY:	PRT:	133 AA.
AC	09PMW7:			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	Ribonuclease precursor.			
GN	RCR.			
OS	Rana catesbeiana (Bull frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.			
OX	NCBI_TaxID=8400;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER:			
RX	MEDLINE-98165825; PubMed-9497370;			
RA	Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;			
RT	"The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.			
RT	Tissue distribution, cloning, purification, cytotoxicity, and active			
RT	residues for RNase activity.";			
RL	J. Biol. Chem. 273:6395-6401(1998).			
DR	EMBL: AF039104; AAD10702.1; .			
DR	HSSP; P11916; 1BC4.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; RNaseA; 1.			
DR	ProDom: PD000535; RNaseA; 1.			
DR	SMART; SM00092; RNase_Pc; 1.			
DR	PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.			
FW	Signal.			
FT	SIGNAL. 1 22	POTENTIAL.		
FT	CHAIN 23 133	RIBONUCLEASE.		
SO	SEQUENCE 133 AA: 14762 MW: A7D62594F7D16F0C CRC64;			
	Query Match 96.6%; Score 585.5; DB 13; Length 133;			
	Best Local Similarity 98.2%; Pred No. 14e-60;			
	Matches 109; Conservative 0; Mismatches 1; Indels 1; Gaps 1			

Db 23 QNATFOCKHIINPTIINCNTIMDNNTIYVGGCKRVYTFIISATTVKAICTGVIMNV 82  
 OY 61 LSTTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQYPVHFAGIGRC 111  
 Db 83 LSTTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQYPVHFAGIGRC 133

## RESULT 2

O98SMO PRELIMINARY: PRT: 133 AA.  
 AC O98SMO;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE RNase A-type ribonuclease rc208 precursor.  
 OS Rana catesbeiana (bull frog).  
 OC Eukaryota: Metazoa: Chordata: Cranialata: Vertebrata: Euteleostomi:  
 OC Amphibia: Batrachia: Anura: Neobatrachia: Ranoidae: Ranidae: Rana.  
 NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21539506; PubMed-11683320;  
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;  
 RT "Rapid diversification of RNase A superfamily ribonuclease from the  
 bullfrog, Rana catesbeiana."  
 RL J. Mol. Evol. 53:31-38(2001).  
 DR EMBL: AF351209; AAK30255.1; -  
 DR HSSP: P11916; IBC4  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC; UNKNOWN\_1.  
 KW Signal.

FT SIGNAL 1 22 POTENTIAL.  
 SQ SEQUENCE 133 AA; 14628 MW; 87FCF12C3499E02 CRC64;

Query Match 91.5%; Score 554.5; DB 13; Length 133;  
 Best Local Similarity 93.7%; Pred. No. 5,7e-57;  
 Matches 104; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

OY 2 QNATFOCKHIINPTIINCNTIMDNNTIYVGGCKRVYTFIISATTVKAICTGVIMNV 60  
 Db 23 QNATFOCKHIINPTIINCNTIMDNNTIYVGGCKRVYTFIISATTVKAICTGVIMNV 82  
 OY 61 LSTTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQYPVHFAGIGRC 111  
 Db 83 LSTTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQYPVHFAGIGRC 133

## RESULT 3

O98SM2 PRELIMINARY: PRT: 132 AA.  
 AC O98SM2;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).  
 OS Rana catesbeiana (bull frog).  
 OC Eukaryota: Metazoa: Chordata: Cranialata: Vertebrata: Euteleostomi:  
 OC Amphibia: Batrachia: Anura: Neobatrachia: Ranoidae: Ranidae: Rana.  
 NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21539506; PubMed-11683320;  
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;  
 RT "Rapid diversification of RNase A superfamily ribonuclease from the  
 bullfrog, Rana catesbeiana."  
 RL J. Mol. Evol. 53:31-38(2001).  
 DR EMBL: AF351209; AAK30255.1; -  
 DR HSSP: P11916; IBC4  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC; UNKNOWN\_1.  
 KW Signal.

FT SIGNAL 1 22 POTENTIAL.  
 SQ SEQUENCE 133 AA; 14615 MW; C8785B236B26E54E CRC64;  
 Query Match 78.0%; Score 472.5; DB 13; Length 133;  
 Best Local Similarity 77.5%; Pred. No. 2.1e-47;  
 Matches 86; Conservative 11; Mismatches 13; Indels 1; Gaps 1;  
 OY 2 QNATFOCKHIINPTIINCNTIMDNNTIYVGGCKRVYTFIISATTVKAICTGVIMNV 60  
 Db 23 QNATFOCKHIINPTIINCNTIMDNNTIYVGGCKRVYTFIISATTVKAICTGVIMNV 82  
 OY 61 LSTTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQYPVHFAGIGRC 111  
 Db 83 LSTTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQYPVHFAGIGRC 133

RP SEQUENCE FROM N.A.  
 RT TISSUE=LIVER;

RA Liao Y.-D., Tang P.-C., Jeng J.-T.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF351207; AAK30253.1; -  
 DR EMBL: AF359578; AAL87036.1; -  
 DR HSSP: P11916; IBC4  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC; UNKNOWN\_1.  
 KW Signal.

FT SIGNAL 1 22 POTENTIAL.  
 FT CHAIN 23 132 RC-RNASE7.  
 SQ SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;

Query Match 79.5%; Score 481.5; DB 13; Length 132;  
 Best Local Similarity 82.7%; Pred. No. 1.9e-48;  
 Matches 91; Conservative 5; Mismatches 13; Indels 1; Gaps 1;

OY 2 QNATFOCKHIINPTIINCNTIMDNNTIYVGGCKRVYTFIISATTVKAICTGVIMNV 60  
 Db 23 QNATFOCKHIINPTIINCNTIMDNNTIYVGGCKRVYTFIISATTVKAICTGVIMNV 82  
 OY 61 LSTTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQYPVHFAGIGRC 110  
 Db 83 LSTTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQYPVHFAGIGRC 132

## RESULT 4

O98SL9 PRELIMINARY: PRT: 133 AA.  
 AC O98SL9;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE RNase A-type ribonuclease rc212 precursor.  
 OS Rana catesbeiana (bull frog).  
 OC Eukaryota: Metazoa: Chordata: Cranialata: Vertebrata: Euteleostomi:  
 OC Amphibia: Batrachia: Anura: Neobatrachia: Ranoidae: Ranidae: Rana.  
 NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21539506; PubMed-11683320;  
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;  
 RT "Rapid diversification of RNase A superfamily ribonuclease from the  
 bullfrog, Rana catesbeiana."  
 RL J. Mol. Evol. 53:31-38(2001).  
 DR EMBL: AF351210; AAK30256.1; -  
 DR HSSP: P11916; IBC4  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC; UNKNOWN\_1.  
 KW Signal.

FT SIGNAL 1 22 POTENTIAL.  
 SQ SEQUENCE 133 AA; 14615 MW; C8785B236B26E54E CRC64;

Query Match 78.0%; Score 472.5; DB 13; Length 133;  
 Best Local Similarity 77.5%; Pred. No. 2.1e-47;  
 Matches 86; Conservative 11; Mismatches 13; Indels 1; Gaps 1;

OY 2 QNATFOCKHIINPTIINCNTIMDNNTIYVGGCKRVYTFIISATTVKAICTGVIMNV 60  
 Db 23 QNATFOCKHIINPTIINCNTIMDNNTIYVGGCKRVYTFIISATTVKAICTGVIMNV 82  
 OY 61 LSTTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQYPVHFAGIGRC 111  
 Db 83 LSTTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQYPVHFAGIGRC 133

## RESULT 5

O98SL8





## RESULT 13

RA Kinoshita N., Kirschner M.W.;

